ADVANCEMENT REPORT ON POPULATION GENETIC STUDY OF BROWN HARE (*Lepus europaeus*) POPULATIONS IN CENTRAL- AND EASTERN-EUROPEAN REGION

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The present phylogenetic status of most European mammal species is eminently the result of the last Pleistocene glaciation. In the case of brown hare (*Lepus europaeus* Pall.) in addition to that more recent effects such as fragmentation of natural habitats, hybridization among different *Lepus* species or competition for decreased food resources should also be considered. The brown hare is present all over Europe from Spain to Asia Minor and is an important game species which makes it a reasonable subject for population genetic researches.

The purpose of our study is to gather data on the genetic diversity of Central- and Eastern-European brown hare populations with the aim of revealing the genetic history of the species in the studied region, from which data are scarce despite the fact that the species is well-studied on the whole continent.

In our research mtDNA cyt*b* and D-loop regions along with the MC1R and ASIP genes are going to be studied. Until now 179 samples have been collected from different countries of Europe and Georgia. 50 of them, originated from Hungary (n = 14) and Serbia (n = 36), have already been sequenced and analysed for the D-loop region. Based on a 411 bp alignment we found a high level of haplotype diversity (Hd = 0.958) with an overall 30 haplotypes, and the nucleotid diversity of $\pi = 0.0167$.

Our ongoing research shows high genetic diversity of the brown hare in the studied region and indicates genetic distinction among the studied populations though these results need confirmation by further studies.

Keywords: brown hare, mitochondrial DNA, diversity, Central Europe, Eastern Europe

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